

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Lyman, Stewart D.  
Beckmann, M. Patricia

(ii) TITLE OF INVENTION: Ligands for flt3 Receptors

(iii) NUMBER OF SEQUENCES: 8

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
(B) STREET: 51 University Street  
(C) CITY: Seattle  
(D) STATE: Washington  
(E) COUNTRY: US  
(F) ZIP: 98101

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Apple Macintosh  
(C) OPERATING SYSTEM: Macintosh 7.0.1  
(D) SOFTWARE: Microsoft Word, Version #5.1

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: -to be assigned-  
(B) FILING DATE: March 7, 1994  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/162,407  
(B) FILING DATE: December 3, 1993  
(C) CLASSIFICATION:

## (viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/111,758  
(B) FILING DATE: August 25, 1993  
(C) CLASSIFICATION:

## (ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/106,463  
(B) FILING DATE: August 12, 1993  
(C) CLASSIFICATION:  
  
(x) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/068,394  
(B) FILING DATE: May 24, 1993  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Malaska, Stephen L.  
(B) REGISTRATION NUMBER: 32,655  
(C) REFERENCE/DOCKET NUMBER: 2813-D

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 587-0430  
(B) TELEFAX: (206) 233-0644  
(C) TELEX: 756822

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 879 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: cDNA to mRNA
  
- (iii) HYPOTHETICAL: NO
  
- (iv) ANTI-SENSE: NO
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..25
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 855..879
  
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 57..752

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACTGGA	ACGAGACGAC	CTGCTCTGTC	ACAGGCATGA	GGGGTCCCCG	GCAGAG	56											
ATG	ACA	GTG	CTG	GCG	CCA	GCC	TGG	AGC	CCA	AAT	TCC	TCC	CTG	TTG	CTG		104
Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Asn	Ser	Ser	Leu	Leu	Leu		
1			5					10					15				
CTG	TTG	CTG	CTG	AGT	CCT	TGC	CTG	CGG	GGG	ACA	CCT	GAC	TGT	TAC		152	
Leu	Leu	Leu	Leu	Ser	Pro	Cys	Leu	Arg	Gly	Thr	Pro	Asp	Cys	Tyr			
							20	25		30							
TTC	AGC	CAC	AGT	CCC	ATC	TCC	TCC	AAC	TTC	AAA	GTG	AAG	TTT	AGA	GAG	200	
Phe	Ser	His	Ser	Pro	Ile	Ser	Ser	Asn	Phe	Lys	Val	Lys	Phe	Arg	Glu		
35					40						45						
TTG	ACT	GAC	CAC	CTG	CTT	AAA	GAT	TAC	CCA	GTC	ACT	GTG	GCC	GTC	AAT	248	
Leu	Thr	Asp	His	Leu	Leu	Lys	Asp	Tyr	Pro	Val	Thr	Val	Ala	Val	Asn		
						50	55			60							
CTT	CAG	GAC	GAG	AAG	CAC	TGC	AAG	GCC	TTG	TGG	AGC	CTC	TTC	CTA	GCC	296	
Leu	Gln	Asp	Glu	Lys	His	Cys	Lys	Ala	Leu	Trp	Ser	Leu	Phe	Leu	Ala		
						65	70		75				80				
CAG	CGC	TGG	ATA	GAG	CAA	CTG	AAG	ACT	GTG	GCA	GGG	TCT	AAG	ATG	CAA	344	
Gln	Arg	Trp	Ile	Glu	Gln	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln		
						85		90		95							
ACG	CTT	CTG	GAG	GAC	GTC	AAC	ACC	GAG	ATA	CAT	TTT	GTC	ACC	TCA	TGT	392	
Thr	Leu	Leu	Glu	Asp	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Ser	Cys		
						100		105		110							

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
      1           5           10          15

Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
      20          25          30

Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
      35          40          45

Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
      50          55          60

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Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala  
65 70 75 80

Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln  
85 90 95

Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys  
100 105 110

Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile  
115 120 125

Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro  
130 135 140

Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln  
145 150 155 160

Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala  
165 170 175

Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu  
180 185 190

Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp  
195 200 205

Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly  
210 215 220

Val Pro Leu Pro Ser His Pro  
225 230

## (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

## (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

**AGCAGGTCGT CTCGTTCCAG**

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 30..734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCCGGAAT TCCGGGGCCC CCGGCCGAA ATG ACA GTG CTG GCG CCA GCC TGG 53  
Met Thr Val Leu Ala Pro Ala Trp  
1 5

```

AGC CCA ACA ACC TAT CTC CTC CTG CTG CTG CTG AGC TCG GGA CTC      101
Ser Pro Thr Thr Tyr Leu Leu Leu Leu Leu Leu Ser Ser Gly Leu
          10           15           20

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AGT GGG ACC CAG GAC TGC TCC TTC CAA CAC AGC CCC ATC TCC TCC GAC 149
Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
   25          30          35          40

```

TTC GCT GTC AAA ATC CGT GAG CTG TCT GAC TAC CTG CTT CAA GAT TAC 197  
 Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr  
                 45             50             55

CCA GTC ACC GTG GCC TCC AAC CTG CAG GAC GAG GAG CTC TGC GGG GGC 245  
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly  
60 65 70

CTC TGG CGG CTG GTC CTG GCA CAG CGC TGG ATG GAG CGG CTC AAG ACT 293  
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr

GTC GCT GGG TCC AAG ATG CAA GGC TTG CTG GAG CGC GTG AAC ACG GAG 341  
 Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu

ATA CAC TTT GTC ACC AAA TGT GCC TTT CAG CCC CCC CCC AGC TGT CTT 389  
 Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu

CGC TTC GTC CAG ACC AAC ATC TCC CGC CTC CTG CAG GAG ACC TCC GAG Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu 125 130 135	437
CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC CGG Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg 140 145 150	485
TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC CCA Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro 155 160 165	533
5 TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro 170 175 180	581
CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC Pro Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala 185 190 195 200	629
GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg 205 210 215	677
CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu 220 225 230	725
G TG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC Val Glu His 235	774
GCAGTGAGAC AGACATCTAT CATCCCATT TACAGGGGAG GATACTGAGG CACACAGAGG 834 GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC 894 CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC 954 GGCCCCATTT ACCCAAATCT GAACAAAGCC CCCG	988

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 235 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu 1 5 10 15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe 20 25 30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
     35                        40                        45  
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
     50                        55                        60  
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
     65                        70                        75                        80  
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
     85                        90                        95  
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
     100                       105                       110  
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
     115                       120                       125  
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
     130                       135                       140  
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
     145                       150                       155                       160  
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala  
     165                       170                       175  
 Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu  
     180                       185                       190  
 Pro Val Gly Leu Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln  
     195                       200                       205  
 Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val  
     210                       215                       220  
 Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His  
     225                       230                       235

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA to mRNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT 60  
 ACTTCAGCCA C 71

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCGAGGCT CTGGGAG

37